Please replace the paragraph beginning on page 6, line 20, with the following rewritten paragraph:

Figure 3. A. Amino acid sequence of human and rat CLASP proteins. Sequences were aligned using ClustalW. One letter amino acid abbreviation used. Protein motifs are found within the labeled boxes. "-" indicates gaps that are placed to acquire a best overall alignment. Other abbreviations: "HC2A" Human CLASP-2 sequence (SEQ ID NO:9), "KIAA" KIAA1058 sequence (SEQ ID NO:10) (Genbank Accession No. AB028981), "rat" TRG gene (SEQ ID NO11) (Genbank Accession No. X68101), "HC4" Human CLASP-3 sequence (SEQ ID NO:12), "HC1" Human CLASP-1 sequence (SEQ ID NO:13), "HC3" Human CLASP-3 sequence (SEQ ID NO:14), "HC5" Human CLASP-3 sequence (SEQ ID NO:15). B. Alignment of DOCK motifs found within the human CLASPs and KIAA0716 (SEQ ID NOS:16-20, 24, 25, 27-43, 47 and 49-55) and compared to canonical DOCK motifs (SEQ ID NO:21-23, 32-34, 44-46 and 56-58). Consensus amino acids found within all DOCK motifs are also indicated.

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Please replace the paragraph beginning on page 12, line 32, with the following rewritten paragraph:

Another preferred example of algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al., 1977, Nuc. Acids Res. 25:3389-3402 and Altschul et al., 1990, J. Mol. Biol. 215:403-410, respectively. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the world wide website of the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always>0) and N (penalty score for mismatching residues; always<0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls

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off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, 1989, Proc. Natl. Acad. Sci. U.S.A. 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

C3

IN THE CLAIMS

Please amend claims 1, 2, 4, 9, 13 and 30. Claims not amended or canceled are reiterated for the Examiner's convenience.

C4

1. **(twice amended)** An isolated Cadherin-like asymmetry protein-3 (CLASP-3) polynucleotide, wherein said polynucleotide encodes at least 200 contiguous amino acids of SEQ ID NO:2 or a biologically active variant thereof.

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2. **(amended)** The polynucleotide of claim 1, wherein said polynucleotide encodes at least 200 contiguous amino acids of SEQ ID NO:2 or an allelic variant thereof.

3. **(reiterated)** The isolated polynucleotide of claim 1, comprising the cDNA coding sequence of ATCC accession numbers PTA-1564, PTA-1570, PTA-2616 or PTA-2617.

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4. **(amended)** An isolated CLASP-3 polynucleotide comprising a nucleotide sequence that has at least 90% percent identity to SEQ ID NO:1 or an allelic variant thereof.

6. **(reiterated)** A vector comprising the polynucleotide of claim 1.

7. **(reiterated)** An expression vector comprising the polynucleotide of claim 1 in which the nucleotide sequence of the polynucleotide is operatively linked with a regulatory sequence that controls expression of the polynucleotide in a host cell.